Abstracts

Publication no. C-1997-0812-04R | VIEW ARTICLE

Thermal Properties of Corn Starch Extraction Intermediates by Differential Scanning Calorimetry (1).

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Thermal properties of corn starch extraction intermediates from four types of corn were studied using differential scanning calorimetry. Starch at four different stages of extraction, including a standard single-kernel starch isolation procedure and three starch extraction intermediates, was isolated from mature corn kernels of B73 and Oh43 inbreds and the mutants of *waxy* (*wx*) and *amylose extender* (*ae*) in an Oh43 background. Differences in thermal properties and moisture and protein contents of starch from the extraction stages were statistically analyzed. Most thermal properties (gelatinization and retrogradation onset temperatures, gelatinization and retrogradation ranges, gelatinization and retrogradation peak temperatures, gelatinization and retrogradation enthalpies, peak height index, and percentage of retrogradation) of starches extracted at stage 3 intermediate (a procedure that did not include a final washing step) were similar to those of starch extracted by the standard single-kernel isolation procedure. Values for gelatinization peak temperature, gelatinization enthalpy, and peak height index were different between the standard and the stage 3 intermediate. The values obtained from starches extracted at stage 3, however, were consistent and predictable, suggesting that this extraction intermediate might be used in screening programs in which many starch samples are evaluated. By using the stage 3 extraction, samples could be evaluated in three rather than four days and the procedure saved approximately equals 0.5 hr of labor time. The other two starch extraction intermediates, which excluded filtering and washing or filtering, washing, and steeping, produced starch with thermal properties generally significantly different from starch extracted by the standard single-kernel isolation procedure.

Evaluation of GEM Experimental Crosses for Starch Amylose

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Dr. Mark Campbell, Faculty Mentor. GEM Cooperators' Meeting. American Seed Trade Association, 1999. Chicago, IL.

Breeding for high-amylose corn starch requires a rapid analytical method for determining starch amylose so that generating wet chemistry values does not pose a major limitation in the volume of materials that can be screened. Two recently described methods for determining apparent amylose were examined and compared to an earlier described iodine-binding method using isolated starch (method 1). These methods included one based on near-infrared transmittance spectroscopy (NITS) (method 2) and another iodine-binding method involving the solubilizing of starch from ground whole corn with a DMSO-iodine solution (method 3). These methods were chosen because, aside from initial set up costs, they are relatively rapid and inexpensive to perform. The materials evaluated consist of 155 different exotic populations including various plant introductions and experimental materials generated from the Germplasm Enhancement of Maize (GEM) project. Crosses were made between these materials and a Corn Belt dent hybrid (OH43 x H99) converted with the amylose-extender (ae) allele. F3 ears, presumed to be homozygous for the ae allele based on visual selection of the seed from which they were planted, were then evaluated in order to identify possible modifiers of ae conditioning high starch amylose. A core set consisting of 155 samples were selected (on F3 ear per exotic cross) from a total of 1006 ear samples harvested which were all subjected to starch amylose analysis using the three methods. The NITS method showed poor correlation to method 1 ($r = 0.88$) however NITS did appear to discriminate between samples having been converted to ae versus those having a normal or possibly segregating endosperm type. Method 3 showed a much better correlation with method 1 ($r = 0.92$) and appeared to better discriminate among samples having apparent amylose AA values >65% from those at or near 55%. Results from this study suggest that NITS may be useful when a quick screening method is needed to discriminate mutant from non-mutant genotypes especially when visual identification is difficult. In addition, method 3 could be used to replace the more time-consuming method 1 when trying to identify high AA levels among ae genotypes even though some inconsistency was observed between the two methods. Finally, this study revealed that exotic germplasm may be an important source of modifiers to the ae allele since values as high as 70% AA were identified.